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TECH CENTER 1600/2900

FIG. 5A

M	N	L/F	P	S	T	K	V	P	W	A	A	V	T	L	L
ATG	AAC	CTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
ATG	AAC	TTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
		*													
L	L	L	L	L	P	P	A	L	L	S	L	G	V	D	A
CTG	CTG	CTA	CTG	CTG	CCG	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCG
CTG	CTG	CTA	CTG	CTG	CCA	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCA
															*
Q	P	L	P	D	C	C	R	Q	K	T	C	S	C	R	L
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
Y	E	L	L	H	G	A	G	N	H	A	A	G	I	L	T
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCC	GCG	GGC	ATC	CTC	ACT
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCT	GCG	GGT	ATC	CTG	ACT
										*		*		*	
L	G	K	R	R	P	G	P	P	G	L	Q	G	R	L	Q
CTG	GGA	AAG	CGG	CGA	CCT	GGA	CCC	CCA	GGC	CTC	CAA	GGA	CGG	CTG	CAG
CTG	GGA	AAG	CGG	CGG	CCT	GGA	CCT	CCA	GGC	CTC	CAG	GGA	CGG	CTG	CAG
				*			*				*				
R	L	L	Q	A	N	G	N	H	A	A	G	I	L	T	M
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
G	R	R	A	G	A	E	L	E	P	Y/H	P	C	P/S	G	R
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	TAT	CCC	TGC	CCT	GGT	CGC
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	CAT	CCC	TGC	TCT	GGT	CGC
									*			*			
R/G	C	P	T	A/V	T	A/T	T	A	L	A	P	R	G	G	S
CGC	TGT	CCG	ACT	GCA	ACC	GCC	ACC	GCT	TTA	GCG	CCC	CGG	GGC	GGA	TCC
GGC	TGT	CCG	ACC	GTA	ACT	ATC	ACC	GCT	TTA	GCA	CCC	CGG	GGA	GGG	TCC
*			*	*	*	*			*			*	*	*	
R/G	V														
AGA	GTC	TGA													
GGA	GTT	TGA													
*															

FIG. 5B

consensus:	RL LL GNHAAGILT G
hcrt1:	LGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
hcrt2:	PGPPGLQGRLLQRLQANGNHAAGILTMG
SECRETIN:	HSDGTFTSKLSRLRDSARLQRLQLGLV HSDGTFTSK
	* * * * *

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PROPOSED AMENDMENTS TO FIG. 5A

FIG. 5A

M	N	L/F	P	S	T	K	V	P	W	A	A	V	T	L	L
ATG	AAC	CTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
ATG	AAC	TTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
		*													
L	L	L	L	L	P	P	A	L	L	S	L	G	V	D	A
CTG	CTG	CTA	CTG	CTG	CCG	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCG
CTG	CTG	CTA	CTG	CTG	<del>CCG</del>	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCA
					CCA										*
Q	P	L	P	D	C	C	R	Q	K	T	C	S	C	R	L
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
Y	E	L	L	H	G	A	G	N	H	A	A	G	I	L	T
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCC	GCG	GGC	ATC	CTC	ACT
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCT	GCG	GGT	ATC	CTG	ACT
										*		*		*	
L	G	K	R	R	P	G	P	P	G	L	Q	G	R	L	Q
CTG	GGA	AAG	CGG	CGA	CCT	GGA	CCC	CCA	GGC	CTC	CAA	GGA	CGG	CTG	CAG
CTG	GGA	AAG	CGG	CGG	CCT	GGA	CCT	CCA	GGC	CTC	CAG	GGA	CGG	CTG	CAG
			*				*			*					
R	L	L	Q	A	N	G	N	H	A	A	G	I	L	T	M
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
G	R	R	A	G	A	E	L	E	P	Y/H	P	C	P/S	G	R
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	TAT	CCC	TGC	CCT	GGT	CGC
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	CAT	CCC	TGC	TCT	GGT	CGC
										*		*			
R/G	C	P	T	A/V	T	A/T	T	A	L	A	P	R	G	G	S
CGC	TGT	CCG	ACT	GCA	ACC	GCC	ACC	GCT	TTA	GCG	CCC	CGG	GGC	GGA	TCC
GGC	TGT	CCG	ACC	GTA	ACT	<del>ACC</del>	ACC	GCT	TTA	GCA	CCC	CGG	GGA	GGG	TCC
*			*	*	*	*				*		*	*	*	
R/G	V							ATC							
AGA	GTC	TGA													
GGA	<del>GTC</del>	TGA													
*	GTT														

FIG. 5B

consensus:	RL LL GNHAAGILT G
hcrt1:	LGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
hcrt2:	PGPPGLQGRLLQRLQLQANGNHAAGILTMG
SECRETIN:	HSDGTFTSKLSRLRDSARLQRLQLGLV HSDGTFTSK
	* * * * *

# FIG. 5A

M	N	L/F	P	S	T	K	V	P	W	A	A	V	T	L	L
ATG	AAC	CTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
ATG	AAC	TTT	CCT	TCT	ACA	AAG	GTT	CCC	TGG	GCC	GCC	GTG	ACG	CTG	CTG
		*													
L	L	L	L	L	P	P	A	L	L	S	L	G	V	D	A
CTG	CTG	CTA	CTG	CTG	CCG	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCG
CTG	CTG	CTA	CTG	CTG	CCG	CCG	GCG	CTG	CTG	TCG	CTT	GGG	GTG	GAC	GCA
															*
Q	P	L	P	D	C	C	R	Q	K	T	C	S	C	R	L
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
CAG	CCT	CTG	CCC	GAC	TGC	TGT	CGC	CAG	AAG	ACG	TGT	TCC	TGC	CGT	CTC
Y	E	L	L	H	G	A	G	N	H	A	A	G	I	L	T
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCC	GCG	GGC	ATC	CTC	ACT
TAC	GAA	CTG	TTG	CAC	GGA	GCT	GGC	AAC	CAC	GCT	GCG	GGT	ATC	CTG	ACT
L	G	K	R	R	P	G	P	P	G	L	Q	G	R	L	Q
CTG	GGA	AAG	CGG	CGA	CCT	GGA	CCC	CCA	GGC	CTC	CAA	GGA	CGG	CTG	CAG
CTG	GGA	AAG	CGG	CGG	CCT	GGA	CCT	CCA	GGC	CTC	CAG	GGA	CGG	CTG	CAG
				*											
R	L	L	Q	A	N	G	N	H	A	A	G	I	L	T	M
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
CGC	CTC	CTT	CAG	GCC	AAC	GGT	AAC	CAC	GCA	GCT	GGC	ATC	CTG	ACC	ATG
G	R	R	A	G	A	E	L	E	P	Y/H	P	C	P/S	G	R
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	TAT	CCC	TGC	CCT	GGT	CGC
GGC	CGC	CGC	GCA	GGC	GCA	GAG	CTA	GAG	CCA	CAT	CCC	TGC	TCT	GGT	CGC
R/G	C	P	T	A/V	T	A/T	T	A	L	A	P	R	G	G	S
CGC	TGT	CCG	ACT	GCA	ACC	GCC	ACC	GCT	TTA	GCG	CCC	CGG	GGC	GGA	TCC
GGC	TGT	CCG	ACC	GTA	ACT	ACC	ACC	GCT	TTA	GCA	CCC	CGG	GGA	GGG	TCC
*				*	*	*	*			*			*	*	
R/G	V														
AGA	GTC	TGA													
GGA	GTC	TGA													
*															

# FIG. 5B

consensus:	RL LL GNHAAGILT G
hert1:	LGVDAQPLPDCCRQKTCSCRLYELLHGAGNHAAGILTLG
hert2:	PGPPGLQGRLLQRLLOANGNHAAGILTMG
SECRETIN:	HSDGTFTSKLSRLRDSARLQRLLOGLV HSDGTFTSK
	* ***** ** ** *

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1 GCTAGGAGACATTGCGGCGGCGGTGGCGGCGTTGGCAGCAGCTGCAGACATGCTGCTGCT 60  
 -----+-----+-----+-----+-----+-----+-----+  
 CGATCCTCTGTAAACGCCGCCGCCACCGCCGCAACCGTCGTCGACGTCTGTACGACGACGA  
 M L L L

61 CAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGG 120  
 -----+-----+-----+-----+-----+-----+-----+  
 GTTCTTTGTCTGCCTCCTGTAGTCGTACAGATACTCTAGGCCCTCTTCGACCCGAGCCC  
 K K Q T E D I S S V Y E I R E K L G S G

121 TGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAA 180  
 -----+-----+-----+-----+-----+-----+-----+  
 ACGGAAGAGACTCCACTACGACCGGGTCTTTCCCCGAGACGAGTAGAACACCGGGAGTT  
 A F S E V M L A Q E R G S A H L V A L K

181 GTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCAGT 240  
 -----+-----+-----+-----+-----+-----+-----+  
 CACGTAAGGGTTCTTTTCGTGAAGCCCCGTTCCCTCCGGGACCACCTCTTACTCTAGCGTCA  
 C I P K K A L R G K E A L V E N E I A V

241 ACTCCGCAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGACGTCCACGAGAGCCCTTC 300  
 -----+-----+-----+-----+-----+-----+-----+  
 TGAGGCGTCCTAATCGGTGGGGTTGTAACACCGAGACCTCCTGCAGGTGCTCTCGGGAAG  
 L R R I S H P N I V A L E D V H E S P S

301 CCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGAATCATGGA 360  
 -----+-----+-----+-----+-----+-----+-----+  
 GGTAGAGATGAACCGGTACCTCGACCATTGTCCACCACTTGACAACTGGCTTAGTACCT  
 H L Y L A M E L V T G G E L F D R I M E

361 GCGGGGCTCCTACACAGAGAAGGATGCGAGCCACCTTGTAGGGCAGGTCTTGGTGCTGT 420  
 -----+-----+-----+-----+-----+-----+-----+  
 CGCCCCGAGGATGTGTCTTCTTCTACGCTCGGTGGAACATCCCGTCCAGGAACCACGACA  
 R G S Y T E K D A S H L V G Q V L G A V

421 CTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTA 480  
 -----+-----+-----+-----+-----+-----+-----+  
 GAGGATGGAAGTATCGGACCCGTAGCACGTGGCCCTGGAGTTCGGACTTTTGGAGGAGAT  
 S Y L H S L G I V H R D L K P E N L L Y

481 TGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATTCA 540  
 -----+-----+-----+-----+-----+-----+-----+  
 ACGGTGTGGAACCTCCTGAGGTTCTAGTACCAGAGACTGAAACCGGACAGGTTTAAGT  
 A T P F E D S K I M V S D F G L S K I Q

FIG. 6A

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541	AGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAGGATATGTGGCCCCAGAGCTCCT -----+-----+-----+-----+-----+-----+-----+ TCGACCGTTGTACGATCCGTGTCTCGGACACCCTGGGGTCTTATACACCGGGGTCTCGAGGA A G N M L G T A C G T P G Y V A P E L L	600
601	GGAGCAGAAACCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTACAT -----+-----+-----+-----+-----+-----+-----+ CCTCGTCTTTGGGATGCCCTTCCGGCATCTACACACCCGGGACCCACAGTAGAGGATGTA E Q K P Y G K A V D V W A L G V I S Y I	660
661	CCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGAT -----+-----+-----+-----+-----+-----+-----+ GGACGACACACCCATGGGGGGGAAGATACTACTCTCGCTAGGACTTGAGAAGTCGGTCTA L L C G Y P P F Y D E S D P E L F S Q I	720
721	TCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGACATCTCAGAATCAGCCAA -----+-----+-----+-----+-----+-----+-----+ AGACTCCCGGTGCGATGCTCAAAGTGAAGGGAAAACCCTACTGTAGAGTCTTAGTCGGTT L R A S Y E F D S P F W D D I S E S A K	780
781	AGACTTCATTCCGGCACCTTCTGGAACGTGATCCCCAGAAGAGGTTACCTGCCAACAGGC -----+-----+-----+-----+-----+-----+-----+ TCTGAAGTAAGCCGTGGAAGACCTTGCACTAGGGGTCTTCTCCAAGTGGACGGTTGTCCG D F I R H L L E R D P Q K R F T C Q Q A	840
841	CTTACAGCATCTCTGGATCTCTGGGGATGCAGCCTTGGACAGGGACATCCTAGGTTCTGT -----+-----+-----+-----+-----+-----+-----+ GAATGTCGTAGAGACCTAGAGACCCCTACGTCGGAACCTGTCCCTGTAGGATCCAAGACA L Q H L W I S G D A A L D R D I L G S V	900
901	CAGTGAGCAGATCCAGAAGAATTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCAC -----+-----+-----+-----+-----+-----+-----+ GTCACTCGTCTAGGTCTTCTTAAAACGGTCTGCGGACCTTCGCACGTAAGTTACGGTG S E Q I Q K N F A R T H W K R A F N A T	960
961	ATCATTCCCTACGTACATCCGTAAGCTGGGACAGAGCCCAGAGGGTGAGGAGGCCCTCCAG -----+-----+-----+-----+-----+-----+-----+ TAGTAAGGATGCAGTGTAGGCATTCGACCCTGTCTCGGGTCTCCCACTCCTCCGGAGGTC S F L R H I R K L G Q S P E G E E A S R	1020
1021	GCAGGGTATGACCCGTACAGCCACCCAGGCCTTGGGACTAGCCAGTCTCCCAAGTGGTG -----+-----+-----+-----+-----+-----+-----+ CGTCCCATACTGGGCAGTGTCTGGTGGGTCCGGAACCCTGATCGGTGAGAGGGTTACCCAC Q G M T R H S H P G L G T S Q S P K W V	1080

FIG. 6B

1081 ACAACCAGGTGGATGCCAAGGAAGGCCAAGTGGACTGACTCCTAGCTTTTCTTTCTCTCCA 1140  
-----+-----+-----+-----+-----+-----+  
TGTTGGTCCACCTACGGTTCCTTCCGGTTCACCTGACTGAGGATCGAAAAGAAAGGAGGT  
T T R W M P R K A K W T D S

1141 GCCCTTTTGATCTCCTTCCCTGATCCTTGTCCCCGGACTGGCCTCTGTTGGAAAGTCCA 1200  
-----+-----+-----+-----+-----+-----+  
CGGGAAAACCTAGAGGAAGGGACTAGGAACAGGGGGCCTGACCGGAGACAACCTTTCAGGT

1201 AGACCGTGGGTGTGATGCATGGCACTGGGGTATGGGGCTTCCCAAGTATGTCCCCAGCCT 1260  
-----+-----+-----+-----+-----+-----+  
TCTGGCACCCACACTACGTACCGTGACCCCATACCCCGAAGGGTTCATACAGGGGTCTGGA

1261 CTGTCCTTTGTTGCTGCCACCCTCTATGGAAACTGAGGAGGTATTCAAAAATGGATTG 1320  
-----+-----+-----+-----+-----+-----+  
GACAGGAAACAACGACGGTGGGAGATACCTTTGACTCCTCCATAAGTTTTTACCTAAACC

1321 GGGCCATCCTTCTGTCACCTTGACGCACATATGCATTGCGTGGCTGTTCTGTGCTTTGC 1380  
-----+-----+-----+-----+-----+-----+  
CCCGGTAGGAAGGACGTGGAACGTGCGTGATACGTAACGCACCGACAAGACACGAAACG

1381 TGA CTGTGGGTGGTCTGCTTGTGTTGTAGCCCTTTAGTTCCTCCTCTTTCCAACCAATA 1440  
-----+-----+-----+-----+-----+-----+  
ACTGACACCCACCAGGACGAACACAACATCGGGAAATCAAGGAGGAGAAAGGTTGGTTAT

1441 AAGACAAACAGAACAATG 1458  
-----+-----  
TTCTGTTTGTCTTGTTAC

FIG. 6C